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                                                                                                                                                                                                          WO200210413-A1.
                                                                                                                                                                                                                                                                            CFACT1
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New fiber-specific actin promoter from cotton for controlling gene expression in cotton fibers and creating transgenic plants, in par cotton plants, having altered fiber characteristics. particular

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Cheng N,

Liu J;

(MOLE-) INST MOLECULAR AGROBIOLOGY.

Claim 2; Fig 2; 36pp; English.

The present invention relates to the isolation of the cotton fibrespecific actin gene, CFACT1, which includes the promoter sequence. The
cotton CFACT1 gene promoter controls specific gene expression at the
transcriptional level in cotton fibres. It is useful for improving cotton
fibres to create new cotton varieties with high fibre quality and yield,
by gene manipulation methodologies. The promoter is also useful for
creating transgenic plants, particularly cotton, having altered fibre
characteristics, and permits selective expression of a transgene in the
cotton fibre, permitting greater latitude in the types of transgenes

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The present invention describes a method differentiating between haematopoietic conssociated with at least 1 gene and/or the subject. The method comprises contacting biological sample obtained from the subject.
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ating between healthy haematopoietic cells and proliferative aematopoietic cells; for differentiating between acute c leukaemia and acute muelcoencer levels.
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des within the target nucleic acid. ABZ09861 to ABZ11118
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gene ther cytosine Human; WO200277272 Haematopoiet sapiens therapy haema meti topoietic cell proliferation disorder; cytostatic;; lymphocytic leukaemia; acute myelogenous leukaemia;hylation state; gene; ds. A 2 ic cell proliferation disorder related DNA sequence

03-OCT-2002.

₹-2002; 2002WO-EP003401.

26-MAR-2001; 2001US-0278333P

(EPIG-) EPIG ENOMICS AG

Lewin A, Schwope Berlin | Olek A, Þ ㅈ T, Pie Ľij Braun A, Distler J, Gepenbrock C, Adorjan Pipscher E, Maier S, MZiebarth H; Guetig D, Howe A, Mueller P, Grabs G, Lesche R, Le Model F, Mueller V, Otto Mueller J; Leu C.

HPI; 2003-01 8942/01

Detecting and disorders, co distinguishes d differentiating between hematopoietic cell proliferative omprises contacting a target nucleic acid with a reagent to between methylated and non-methylated CpG dinucleotides. that

Claim 28; SE( ID NO 240; 117pp; English.

subject. The biological sawhich disting dinucleotides differentia associated represent invention. differenti present spe at ε invention describes a method for detecting and ing between haematopoietic cell proliferative disorders ith at least 1 gene and/or their regulatory regions in a method comprises contacting a target nucleic acid in a ample obtained from the subject with at least 1 reagent, guishes between methylated and non-methylated CpG is within the target nucleic acid. ABZ09861 to ABZ11118 ecifically claimed nucleotide sequences from the present ligonucleotides from the present invention can be used: ing between healthy haematopoietic cells and proliferative on can be used: fo and proliferative

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RESULT 6
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RESULT 7
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                                                                                                                a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate cells for detecting ;
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01-SEP-2000;
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2000DE-01043826
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  fragment of of diseases
                                                             Berlin
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chemically modified gene, useful associated with abnormal cytosine

ID NO 1542; 32pp + Sequence Listing; German.

sent invention provides a number of human immune system associated hich are modified by the methylation of cytosines. The sequences used in the diagnosis and treatment of immune system disorders, ng eye diseases such as retinopathy, neovascular glaucoma and degeneration, arteriosclerosis, anaemia, cancer, acute myeloid ia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, oid arthritis, psoriasis and inflammatory/ulcerative bowel s. The present sequence is a gene of the invention

11.1%; Score 90.2; DB 6; larity 50.1%; Pred. No. 0.0052; Conservative 0; Mismatches 273; BP; 2163 A; 185 C; 2060 G; 3897 T; 0 U; 0 Other; Length 8305; Indels 10; 2

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AATTCTTAAATATATAAATTTTTTAAAATAGCTTTTCAGTAAATCTGTCAAACAATAGAA
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                                        s of chemically modified genes associated with tumor suppressor denotes on designing primers and probes for analyzing associated with cytosine methylation state e.g. cancer.
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2000DE-01019058.
2000DE-01019173.
2000DE-01032529.
2000DE-01043826.
                                                                                                                                                                                                                                                                              r suppressor gene; oncogene; antitumour; c dinucleotide; single-nucleotide polymorphi
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                                         l probes for analyzing e.g. cancer.
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The inbases

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sequence of 18 DNA) e.g. with

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complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
coligomer (PNA) of at least 9 nucleotides and may form part of a set of
coligomer (PNA) of at least 9 nucleotides and may form part of a set of
currobes for detecting the cytosine methylation state and/or single
nucleotide polymorphisms and also to be used in an array for analysing
diseases associated with CpG dinucleotides e.g. cancers and tumours. The
currobes can also be used in a method for ascertaining genetic and/or
currobes can also be used in a method for ascertaining genetic and/or
currobes can also be used in a method for ascertaining genetic and/or
currobes can also be used in a method for ascertaining genetic and/or
currobes can also be used in a method for ascertaining genetic and/or
currobises or the predisposition to specific diseases, by analysing
currobise methylations. The parameters may be compared to another set of
currobise and/or epigenetic parameters, the differences serving as basis
currobised from tumour suppressor genes and oncogenes. Note: The sequence
currobise patent did not form part of the printed specification, but
currobised in electronic format directly from WIPO at
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Best Local
Matches 2
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No. 0.0069;
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                          identical to a chemically pretreated DNA of genes associated with pharmacogenomics and their complements, arranged in an array for analysing diseases associated with the methylation state (CpG) and detecting SNPs (single nucleotide polymorphisms) of the 87 sequence oligomers may also be used as PCR primers. The set of 87 nucleic and their complements is useful for diagnosis and therapy of solic tumours and cancer. The present sequence represents one the 87 DNF sequences or its complement. Note: The sequence data for this pate not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                               sequences
treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.
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                                                                                                                                                                                                                                                                                                                  comp.
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ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TX
pharmacogenomics; SNP; single nucleotide polymorphism.
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2000DE-01043826.
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ABK40031

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RESULT 13
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leukaemia, Alzheimer's
rheumatoid arthritis, I
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antiarteriosclerotic; antianaemic; cytostat
neuroprotective; anti-HIV; anticonvulsant;
antirheumatic; antiarthritic; antidiabetic,
antiinflammatory; cancer; eye disease; arte
acute myeloid leukaemia; Alzheimer's diseas
neurofibromatosis; rheumatoid arthritis; pa
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                                                     Burger M, Schmitt A;
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; cancer; adenoma; carcinoma; cytosine methylation state;
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Detecting a associated target nucl a reagent.
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nucleic acid in
                    and differentiating between colon cell proliferative disorders d with a gene or its regulatory regions comprises contacting a cleic acid in a biological sample obtained from the subject wit
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with
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32; SEQ ID NO 340; 74pp; Engli

between colon cell proliferative disorders associated with at least one gene or its regulatory regions. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least one least one reagent or a series of reagents, where the reagent or series of connucleotides within the target nucleic acid. The molecules of the invention demonstrate cytostatic activity whilst the method may useful disorders, including cancers such as colon cell proliferative of the PNA (peptide nucleic acid)-oligomers are useful as probes for determining cytosine methylation state or single nucleotide polymorphisms. The current sequence is that of the pretreated genomic DNA region of the invention. This sequence is not shown within the specification but is taken from Wipoweb. DNA 0f

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Sequence 6478 8₽; 1878 Þ 0 C; 1282 G; 3318 ,; H 0 ų; 0 Other

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                   GATTTGTCA
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Nucleic acid diagnosis and methylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              system associated gene SEQ ID NO:
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                                                                                                                                            fragment of chemically modified gene, useful of diseases associated with abnormal cytosine
                                                                                                                                                                                                Berlin K;
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                                                                                                                                                                                                                                                                                                                                                                    bowel disease;
                                                                                                                                                          useful for
                                                                                                                                                                                                                                                                                                                                                                    gene;
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Query Ma Best Loc Matches The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention Sequence Match Similarity 6602 10.8%;
larity 48.8%;
Conservative BP; 4432 A; 202 C; Score 88.2; DB 6; Pred. No. 0.008; 0; Mismatches 308; 3755 G; 8213 T; 0 U; 0 Other; Length 16602; sequences associated

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                                                                    TTTTTTTATTTTGTTATTATATGGGTTAGTTATTGTTTTTGGTTTTAATTAGTGTTGGAG
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Tissue Plasminogen
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RESULT 3
US-08-213-419B-3
; Sequence 3, Applic
; Patent No. 633340;
; GENERAL INFORMATIC
; APPLICANT: Insel;
; TITLE OF INVENTIC
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ORIGINAL SOURCE:
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LENGTH: 6
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-883~795A-3
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STRANDEDNESS: single
TOPOLOGY: linear
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MION: GENE
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et al.
ENCODING PROTEIN ANTIGENS
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OF.

PLASMODIUM FALCIPARUM

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 36:
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REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
GTTTTTATTTTATTTTTCTATTTAGAGAAACTAGAAATTGATTTGTCAAATGTCTTTA
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LICATION DATA:
ON NUMBER: US/08/883,795A
TE: 27-JUN-1997
ATION: 435
                                                                            <u> ATTATTATATATAAATAAATAAATCATTGTAATATGTAAAAATAATTTAAAATA</u>
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Pred. No. 1.7e-06;
D; Mismatches 246;
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CURRENT APPLICATION NUMBER: US/08/213,41
CURRENT FILING DATE: 1994-03-14
PRIOR APPLICATION NUMBER: US 07/870,506
PRIOR FILING DATE: 1992-04-17
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                                            Patent No.
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CANT: Slade, Mar
CANT: Chang, And
CANT: Williams,
F OF INVENTION: I
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Similarity 50.4%;
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(3850)
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                                                                                                     GAAA
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                                                                                                                        GAAA
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LOCATION:
-07-867-106-2
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SOFTWARE:
CURRENT APPL
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PRIOR APPLICATION DATA:
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STATE:
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VICATION INFORMATION:
VE: 215-568-3100
215-568-3439
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SEQUENCES: 19
ENCE ADDRESS:
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iladelphia
 AAGTAAATCATTTTCAGAAAAGTAAATCATTTTTCAGAAATTATTTTTCGGAAATTATTT
                      TTTAAAATTATGTATCGATTTTATTTTAAAATCATTGACGAGATTAAAAATCTTAAAA
                                           TTTCAGTAAATCTGTCAAACAATAGAAAATATTTTTTGCAGGTTCATCCAAACACCAGAA
                                                                ACTCAATCAAACAATAAAAAGATAATAAATTCTTAAATATATAAAATTTTTTAAAATAGCT
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ON NUMBER: PCT/AU90/00530
NTE: 02-NOV-1989
ENT INFORMATION:
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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OR APPLICATION NUMBER: PCT/EP01/03971

OR FILING DATE: 2001-04-06

OR APPLICATION NUMBER: DE 10019058.8

OR FILING DATE: 2000-04-06

OR APPLICATION NUMBER: DE 10019173.8

OR FILING DATE: 2000-04-07

OR APPLICATION NUMBER: DE 10032529.7

OR APPLICATION NUMBER: DE 10032529.7
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AL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: nucleic acid
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TITLE OF INVENTION:
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ATTORNEY/AGENT
NAME: Grave
REGISTRATION
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ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMAT
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
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: (416) 364-7311

(416) 361-1398

DR SEQ ID NO: 36:
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                                                                                                                                                                                      ORGANISM: Artificial
                                                                                                                                                  0-204-708-33
                                                                                                                                                             FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                           ENT FILING DATE: 2003-05-06

R APPLICATION NUMBER: PCT/EP01/03971

R FILING DATE: 2001-04-06

R APPLICATION NUMBER: DE 10019058.8

R FILING DATE: 2000-04-06

DR APPLICATION NUMBER: DE 10019173.8

DR APPLICATION NUMBER: DE 10032529.7

DR APPLICATION NUMBER: DE 10032529.7

DR APPLICATION NUMBER: DE 10032529.7

DR FILING DATE: 2000-06-30
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                        TAGTATTAATTGTGGTTTGGAAGTTAATATATATTATTCAATCCTTGTTTTTTATTTT
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BERLIN, Kurt
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NOS: 98
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                                                                                                  Score 75.8; DB 4;
Pred. No. 2.9e-05;
); Mismatches 312;
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CURRENT APPLICAT
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LENGTH: 615
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                                                                                                                                  TYPE: DNA
                                                                                                  FEATURE:
OTHER INFOR
                                                                                                                        ORGANISM:
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R APPLICATION NUMBER: PCT/EP01/03971

R FILING DATE: 2001-04-06

R APPLICATION NUMBER: DE 10019058.8

R FILING DATE: 2000-04-06

R APPLICATION NUMBER: DE 10019173.8

R APPLICATION NUMBER: DE 10019173.8

R FILING DATE: 2000-04-07

R FILING DATE: 2000-04-07
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HERLIN, Kurt
INVENTION: Diagnosis of Diseases Associat INVENTION: by Assessing DNA Methylation RENCE: 5013.1012
APPLICATION NUMBER: US/10/204,708
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                                         9.3%;
lilarity 49.0%;
Conservative
                                                                                                    chemically treated genomic
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                                              Score 75.6; DB 4;
Pred. No. 3.2e-05;
0; Mismatches 294;
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                                                                       Length 6156;
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FILE REFERENCE: GENES INVOLVED IN ARA;
FILE REFERENCE: GENES INVOLVED IN ARA;
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NITMEET: 1999-03-23
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                                                    TYPE: DNA
ORGANISM: Homo
FEATURE:
NAME/KEY: misc
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                                                                                                                                                       PRIOR
                             LOCATION: 1123..3123
OTHER INFORMATION: 5'regulatory
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                       NAME/KEY:
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FILING DATE: 1999-02-12
INFORMATION:
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LOCATION: 2341
OTHER INFORMATION: 10-512-36:
NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318
NAME/KEY: allele
LOCATION: 2832
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LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorp
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorp
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 : polymorp
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion
NAME/KEY: allele
LOCATION: 1827
COUNTED INFORMATION: 10-510-173 : variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
NAME/KEY: exon
LOCATION: 12254..12340
OTHER INFORMATION: exon 9
NAME/KEY: exon
LOCATION: 12854..13023
OTHER INFORMATION: exon 10
NAME/KEY: exon
LOCATION: 13308..13429
OTHER INFORMATION: exon 11
NAME/KEY
                                                                                                                                                                                               NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62
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LOCATION: 17063
OTHER INFORMATI
                                                                                                                           NAME/KEY: allel
LOCATION: 2341
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OTHER INFORMATION: 10-511-337
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LOCATION: 2323
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OTHER INFORMATI
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OTHER INFORMATION: exon 12
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
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LOCATION: 1656
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LOCATION: 7379..7522
OTHER INFORMATION: exon 7
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LOCATION: 6349..6509
OTHER INFORMATION: exon 6
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LOCATION: 5996..6099
OTHER INFORMATION: exon 5
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LOCATION: 5758..5880
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LOCATION: 5552..5633
OTHER INFORMATION: exon 3
          INFORMATION: 10-513-250
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; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
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RESULT 11
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         Sequence 6, Application Patent No. 6677731 GENERAL INFORMATION:
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LENGTH: 5152
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OR FILING DATE: 2001-04-06
OR APPLICATION NUMBER: DE 10019058.8
OR APPLICATION NUMBER: DE 10019173.8
OR APPLICATION NUMBER: DE 10019173.8
OR FILING DATE: 2000-04-07
OR APPLICATION NUMBER: DE 10032529.7
OR APPLICATION NUMBER: DE 10032529.7
OR FILING DATE: 2000-06-30
OR APPLICATION NUMBER: DE 10043826.1
OR FILING DATE: 2000-09-01
BER OF SEQ ID NOS: 98
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Local Similarity 49.6%;
nes 277; Conservative
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INT APPLICATION NUMBER: US/10/204,708
INT FILING DATE: 2003-05-06
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CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT FILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: PCT/EP01/03971

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10032529.7
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APPLICATION NUMBER: DE 10043826.1
FILING DATE: 2000-09-01
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INVENTION: Diagnosis of Diseases Associated
INVENTION: by Assessing DNA Methylation
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Pred. No. 5.2e-05;
Mismatches 251;
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RESULT 12
US-08-749-391-1
; Sequence 1, Application
; Patent No. 5948667
; GENERAL INFORMATION:

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US/08749391

Kuo-Joan

Leonard

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MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Donna M. Ferber
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT IN
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CORRESPONDENCE ADDRESS:
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IMMEDIATE SOURCE:
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LENGTH: 2058 base pair
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CITY: I
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Liu, Jin-Hao
Hu, Youji
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ilarity 54.7%;
Conservative
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PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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No. 5.1e-05;
smatches 138;
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US-09-390-200-1
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US-09-390-200-1
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                                       Query Match 9.1%;
Best Local Similarity 54.7%;
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/390,200
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/749,391
FILING DATE: 13-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Donna M. Ferber
                                                                                                                                                                                                                                                                                                                                          INFORMATION
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IMMEDIATE S
LIBRARY:
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                                                                                                                                      CLONE:
                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
FORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                            NAME: Donna M. Ferber
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 93
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TOPOLOGY: li
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INVENTION: A Xylanase Obtained From
INVENTION: Anaerobic Fungus
SEQUENCES: 6
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Liu, Jin-Hao
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RESULT 14
US-09-641-638-651
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CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 60/133,200
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                                                                   OTHER INFORMATION: ex
NAME/KEY: exon
LOCATION: 5758..5880
OTHER INFORMATION: ex
NAME/KEY: exon
LOCATION: 5996..6099
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NAME/KEY: misc_feat;
LOCATION: 1123..312;
OTHER INFORMATION: !
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                NAME/KEY:
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LOCATION: 3871..4072
OTHER INFORMATION: exon
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LOCATION: 3124..3297
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LOCATION: 5552..5633
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R APPLICATION NUMBER: US 09
R FILING DATE: 1999-03-23
R APPLICATION NUMBER: US 60
R FILING DATE: 1999-02-12
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NAME/KEY: allele
LOCATION: 2844
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NAME/KEY: allele
LOCATION: 2934
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LOCATION: 1225.
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NAME/KEY: exon
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OTHER INFORMATION: NAME/KEY: allele
LOCATION: 2623
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LOCATION: 1827
OTHER INFORMATION: NAME/KEY: allele
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION:
NAME/KEY: allele
LOCATION: 1559
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NAME/KEY: exon
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LOCATION: 1128
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LOCATION: 1706
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INFORMATION: exon 7
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TON: exon 12
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
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## SUMMARIES

Result

## ALIGNMENTS

REFERENCE AUTHORS TITLE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 AX370648
1 Li,X., Cai,L., Cheng,N. and Liu,J.W. Isolation and characterization of a fiber-specific actin promoter	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Arabidopsis sp.	Arabidopsis sp.		AX370648.1 GI:19168813	AX370648	Sequence 2 from Patent WO0210413.	AX370648 3041 bp DNA linear PAT 01-MAR-2002	

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Methods and nucleic acids for the analysis of hematopoietic cel
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ilarity 53.1%;
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mol_type="unassigned DNA"

db_xref="taxon:32630"

note="chemically treated genor
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Direct Submission

Submitted (10-AUG-2002) Biochimie, Unive Boul. Edouard-Montpetit, Montreal, Quebe On Sep 29, 2002 this sequence version re Location/Qualifiers

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GSREQKITAGYYFFFYTLIGSVLMLIGILYLYSISGTTDYLTLLGYEIDPTAQKYLFL
AFFASLAVKIPKFPFHIWLPQAHVEAPVAGSVILAGILIKLGGYGFIRFTIPLLPDAS
HYFAPLVFILGVLAVIYASLTTLRQTDLKRIIAYSSVSHMGLVSLGIFTLTANGIMGS
IFLQLAHGLVSSALFIIVTVLYDRHHTRLVKYYRGMTVTMPIYSFLFLFFTLANIAVP
LSCNFVGEFLCLLAIFEVNTTVAILASLGIILSACYSLFLYNRVCFGSFSTYLSNNSY
HLLSIKDVSRREFFVLFPLVILTIILGVYPHPIFDLLNISVINLTTFL"
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7006. .700
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7386. .7736
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organelle="mitochondrion"
mol_type="genomic DNA"
strain="ATCC 50154"
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transl_table=
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ILLSVILCVGDINITSIVLAQKNIWFIIPLFPAFIMFLVSALAETNRAPFDLTEGESE
LVSGYNVEYSAIFFTLFFLAEYTHIIFMSILTSLLFFGGWLPPFDFFIFNLIPGEIWL
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MIVIELISHTAKAVSLGVRLAANITAGHILFAILSGFTWTMLTSGGFMIIASLFPMAI
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GFPFLAGFYSKDAILELAYGKYTIDGTFAHLLGTLAAGMTAYYSIRLIYMTFLSDTNG
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/product="NADH dehydrogenase subunit
/product="AAN28343.1"
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467 ATAATAAATTCTTAAATATATAAAATTTTTTAAAATAGCTTTTCAGTAAATCTGTCAAACA 526 	44
407 AAATAATTTAAAATATAAATTTAATATATATAATAAAACTCAATCAAACAATAAAAAA	
347 TTAGTTTAATAATTGAGCATTATTATATATAAATAAATAA	4
287 AACACAATTACAAATAATTTATTTAACTTTGGTTGTTTTCAATTTATGACGGTTAATATT 346 	44
227 AATTGTGGTTTGGAAGTTAATATAATTATTCAATCCTTGTTTTTTTT	
167 AAGTATTTTCATGGAAGGTGTTAAGAATTAATGTTATTGGGATTACTAATTTCTAGTATT 226 	44
ry Match 13.2%; Score 107.4; DB 2; Length 110000; t Local Similarity 49.2%; Pred. No. 0.00013; ches 282; Conservative 0; Mismatches 291; Indels 0; Gaps 0;	8 C A
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706 CAAATGTCTTAATCTAGCTTGTTTAGATTAGTTGAA 742 	7
646 CTAAGTGTTTCTGTTTTTATTTTTATTTTTCTATTTAGAGAAACTAGAAATTGATTTGT 705	7
589 AAATCATTTTCAGAAATTATTTTTCGGAAATTATTTTACTGGCAAACAAA	7
529 AGAAAATATTTTTTGCAGGTTCATCCAAACACCAGAAAAGTAAATCATTTTCAGAAAAGT 588 	~3

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Direct Submission
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University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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Feb 1, 2002 this sequence version sequencing Center
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0038D12
Drafting Center: WIBR
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

SOURCE

INFORMATION:

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The clone sequenced to the left is RP11-680J17; the clone sequenced to the right is RP11-416E16, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-38D12; actual end is at base position 78181 of RP11-416E16.
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                                                                                                                                                                                                                       /rpt_family="Alu"
3535. .3841
/rpt_family="Alu"
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/rpt_family="MER1_type"
7019. .7190
/rpt_family="MIR"
7399. .7794
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9091. .9307
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9343. .9649
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9626. .9649
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13161. .13189
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mol_type="genomic DNA"
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                                            Score 105.2; DB 9;
Pred. No. 0.00025;
0; Mismatches 243;
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FEATURES

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1 (bases 1 to 250029)

Gardner, M.J., Hall, N., Fung, E., White, O., Berriman, M., Hyma Carlton, J.M., Pain, A., Nelson, K.E., Bowman, S., Paulsen, I.T. James, K., Eisen, J.A., Rutherford, K., Salzberg, S.L., Craig, J. Kyes, S., Chan, M.-S., Nene, V., Shallom, S.J., Suh, B., Peters, Angiuoli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.M.A., Fairlamb, A.H., Fraunholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Carrocci and J. Hoffman, S.L., Newbold, C., Davis, R.W., Fraser
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AE014839 AE014186
AE014839.1 GI:234
                                                                                                                   Gardner, M.J.

Direct Submission

Submitted (13-SEP-2002) The
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                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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                               /product="hypothetical protein"
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/protein id="AAN35796.1"
/db xref="GI:23496136"
/translation="MNIFGLLLINLINVIFILCNIKRKNKFLKRQLCSNELKHLKYK
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CLSSSNHISSNMMGNTFYENVYINYLKDYIIDEKEKAMEKNIVKDEEQKKDKIYFPNS
NNMLNAKDIENVIHERIRKEEENLFEFLKSVNERYNLNCTLRVVGGWVRDKFLNIND
DIDITVDNMKGAEFCNYIKEYIKEKENKNFNFGIIKINSDQSKHLETSSFNLFNFQVD
IVNLRNEKYTEESRIPEIVIGTPEEDALRRDFTVNSLFYNLKNKKVEDYTEKGIFHLK
NHIISTPLEPLATFLDDPLRIVRCIRFCGFFNFFLEKSIFNVLKNEDIKKAFTKKISK
SRLSSEIVKIFSAKCKNVILSLTLLNYSSYSSKIFQLPSNYFVKDEELFEKLKKKDKI
NKGIVTPAQHYHTNDSVHDQHVDNLNDLNCVSSNNNINNKKIHLQNVENSNICNNSSN
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LKFPLKYSKFCVHIFEGFTHLYNLYKTIDVLNFLKNKNYQEEHNIQIKGQTVLCLKKI
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/locus_tag="PF11 0211"
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/locus_tag="PF11 0211"
complement (join(8517. .944/
/locus_tag="PF11_0211"</pre>
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join(<11804. .14104,14233.
/locus_tag="PF11_0212"
join(11804. .14104,14233. .1
/locus_tag="PF11_0212"
PFLKWPDIKHNFPNISPNQINEVYEQIIKFMAIHGENEKECIEYLKQHFTK"
14183. .14224
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HLDVHDSILRFWGVENADHNDIDEKNPELFYHKLGEFLSYCSKFNMNE"
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KLQKLSNLLNALRSNIEKILKNETDMKNMYLTTLNKISINKIKDYSDLEILLETHLQL
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IDRELKNILQKEENLQLINEEENIIIEKTKSDKYDEKENKSNDNILSKKHDDENINKS
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/locus_tag="PF11_0213"
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15533. .>22780))
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'db_xref="GI:23496137"
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Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Planck-Institut fuer Biochemie, Am Klopferspitz 18a insried, Germany; E-mail: Mewes@mips.biochem.mpg.de Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submission
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YLQDVQEYKNILGGNIYFDKSQNGYYKWSIQSKDMVLNFINDYIKMNPSRTTKMNKLY
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'transl_table=
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22246,23612. .23746,25318. .25342,26229. .26
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NPGDNGVFMVPKFNLNKVRYFSTLSKLNARKEDSLAYLTKINTTDFSELNKLMENNHN
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TNMFKFSPVRRVEIPKTSGGFRPLSVGNPREKIVQESMRMMLEIIYNNSFSYYSHGFR
PNLSCLTAIIQCKNYMQYCNWFIKVDLNKCFDTIPHNMLINVLNERIKDKGFMDLLYK
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VLVDPHSKVSFSIDDFKIRHKMNMTDSNYTPDEILDRYKYMLPRSLSLFSGICQICGS
KHOLEVHHVEGILNNAANTINFTTLRGRITYILFYSCCLTLARKFKLNTVKKVILKFGK
VLVDPHSKYSSSIDDFKIRHKMNMTDSNYTPDEILDRYKYMLPRSLSLFSGICQICGS
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/note="ORF Q0055"
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IKPLDTSDIGSNAWLAGMTDADGNFSINLMNGKNRSSRAMPYYCLELRQNYQKNSNNN
NINFSYFYIMSAIATYFNVNLYSRERNLNLLVSTNNTYKTYYSYKVMVANTYKNIKVM
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/gene="I-SCEIII"
join(13818. .13986
/gene="I-SCEIII"
/note="ORF Q0060"
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13818. . 16322
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SHLKNTYLENK"
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join(13818. .13986,18954. .19996)
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/gene="SCAI2"
join(13818. .13986,16435.
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Pred. No. 0.00029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .935
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Direct Sul
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Sequencing vector: M13; M77815; 10% of reads
Sequencing vector: plasmid; L08752; 89% of reads
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HTG; HTGS_PHASE1; HTGS_CANCELLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
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1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clasts: clonerequest@sanger.ac.uk
p 9, 2000 this sequence version replaced gi:4688904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens (human)
   3493
3593
                                                           It currently sists of 2 contigs. The true order of the pieces not known and their order in this sequence record is trary. Gaps between the contigs are represented as of N, but the exact sizes of the gaps are unknown. record will be updated with the finished sequence soon as it is available and the accession number will
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Eutheria; Primates; Catarrhini; Hominidae
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ac.uk Clone
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Berlin, K. Olek, A.,
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3593. .47972
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Piepenbrock,
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mol_type="genomic DNA"
db_xref="taxon:9606"
                                construct
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       Braun, A.
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Distler,J.,
C., Adorjan,
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Lewin, A., Lipscher, E., Maier, S., Model Pelet, C. and Ziebarth, H.

Methods and nucleic acids for the anal proliferative disorders

Patent: WO 02077272-A 386 03-OCT-2002;

Epigenomics AG (DE)
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5, A.F.A. & Green, P. (1996-1997)
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Method for the detection of cytosine methylations

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mol_type="unassigned DNA"

db_xref="taxon:32630"

note="lower strand of DNA sequireatment and P CR"
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Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
L Nature 419 (6906), 527-531 (2002)
B. 22355708
D. 1336867
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Barrell,B.
Barrell,B.
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                                                                                  /codon_start=1
/product="hypothetical |
/protein_id="CAD49075.1"
/db_xref="GI:23477009"
/db_xref="SPTREMBL:Q81227"
/translation="MENRSKTISQNTIKAHVEANDECKEKKEKYLKCFNNWYKNNFLK
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complement(join(1392...1461,1752...2598,2748...2848,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing Co
                                                                                                                                                                                                   n 15el..
fasta :
                                                                                                                                                                                                                                                                                                                               pombe hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium
                                                                                                                                                                                                                                                                                                                                                                            .804))
                                                                                                                                                                                                                                                                                                                                                                                                                                           .804))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A., Brooks, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               κ, C.,
, N. a
                                                                                                                                                                                                   scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Harris, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consortium,
on, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2003
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feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="synonym: MAL1P3.01"
complement(join(1392...1461,
2990...3276))
/gene="PFA0580c"
/note="Originally annotated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="MALIP3.02"
/note="synonym: PF
5005. .5496
/gene="MALIP3.02"
/note="contains po
                                                                                                                                                                                                                                                                                                                                               14884. .20352
/gene="MAL1P3.03"
/note="synonym: PF
14884. .20352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains possible signal sequence. Signal peptide predicted SignalP 2.0 HMM (Signal peptide probabilty 0.640, signal anchor probability 0.357) with cleavage signability 0.504 between residues 27 and 28. ScanRegExphit to PS00867, Carbamoyl-phosphate synthase subdomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="PFA0580c"
/note="svno--
                                                                          transporter abc1 abc1 or (SWALL:Q92337) (1427 aa) 21.46% id in 1146 aa"
                                                                                                                                                                                                                                                                      /gene="MAL1P3.03"
/note="Putative ABC
Pfam match to entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MKLLNNRFVVLCPIIILFFFLNSVVLGNNNRNNINFHETENAAKAMRKLLSGEINSIKLDNGDELKIKLNDEKHKDSTKWDKSYSFISNLEEEKYSQTDLFRKKQEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/product="TatD-like deoxyribonuclease, putative"
/protein_id="CAD49076.1"
/db_xref="GI:23477010"
/db_xref="SPTREMBL:Q8I226"
/translation="MKLVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV
/translation="MKLVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV
LQIKKRSNLKKNHNIRKMEDNESSFIDIGSNLTDKMFDGVYNSKKHENDLQNVLNRAK
NNNVDKIIITCTCLAEIDKSLKICETYDPEGKFLYLSAGVHPTNCYEFIDKNKHEEKE
IIAKKEYEEFIKYFKNEQVENSKMENGNKKICDGEKDMNNLNEILLEKNLDTIPGFKY
                                                                                                                                                                                                   ScanRegExp
                                                                                                                                                                                                                            ATPases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signature 2"
                                                                                                                                                       Similar to Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEKDKEYLENLKNKIIKYPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIFQLKLVQMFN
LPMFLHMRNCSETFFKIVDIYKFLFEKNGGVIHSFTDKEDIVHIIVQNYKNLYIGVNG
CSLKSLENINAVKKIPLNLLLLETDAPWCGVKKTHASYEYIKDTYEKRAYTNLKKIKN
IIKCDDNTIFKERNEPYNIADIAEITYKVREEAVPFDLFCKK"
                    /codon_start=
/product="ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
product="hypothetical;
protein_id="CAB63557.1
db_xref="GI:6594245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xref="GOA:Q9U0N5"
xref="SPTREMBL:Q9U0N5"
                                                                                                                                                                                                                                                 45.00,
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                                                                                                                                                                                                                        Putative ABC transporter
tch to entry PF00005 ABC tran, ABC transporter,
5.00, E-value 1.7e-09; HMMSmart hit to SM00382,
associated with a variety of cellular activities;
:"ABC transporter,
_id="CAB63558.1"
                                                                                                                                                                                                       hit
                                                                                                                                                                                                  to PS00211,
                                                                                                                                                                                                                                                                                                                                                                           PFA0590w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    centromere"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFA0585w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein"
1"
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                                                                               spac9e9.12C teasta scor
                                                                                                                                                                                                       ABC
                       putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2598,2748.
                                                                                               : ATP-binding
: SWALL:ABC1_S
:s: E(): 4.2e-
                                                                                                      4.2e-08,
                                                                                                                                                                                                 family
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Local Similarity
CAATCCTTGTTTTTTTTTTTTTTTTATAACACAATTACAAATAATTTATTTAACTTTGG
                                                                                                        TGAAAATGTTAATGGTAGTGCTATGTCGAAGTATTTTCATGGAAGGTGTTAAGAATTAAT
                                                      ATTATATATTATTAA
                                                                                                                                                                  12.5%; ilarity 51.4%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IILIYFFVFKRFSRGCKEAQRLYLSCHTPLCNIYSNALSGKNIINIYKKNTYHLDVYE
HYINNFRISYFFKWLINIWASLYIKIFILLLTTYIIMHPHLYASGIIKLYKEKNYVRI
LSTLGYCISFSARLGVIIKFLLCDYTHIEKEMCCVQRLEEFAKISNKENASMNKENEL
NVITTQTYKEKNENISDKISAIVEYKNVSLSSIINSSQDDESKKKYGIKFENVYVSYK
KKIPLVNGTYKYIDEEPSLKNINMYALKNQKIGIVGKSGAGKSTILLSILGLINISQG
KITVEGRDIRTYNRKGEDSIIGILAQSSFVFYNWNIRTFIDPYNNFTDDEIVHALKLN
GINLGKNDLYKYMHKQDMKSNYKKIIQTSKVINQSNDNTILLTNDCIRYLSLVRLYLN
RHKYKIILIDEIPIFNLNNSVHDELNSFLIGKAKSFNYIIRNHFPNNTVLIISHHANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLDNFLIEDILDNVQYEVNIFEIQDKTLKYRGNISEYMEKNNLNITKESHWGYSNLNT
IDYTRIKLFDEVELNHVKHSNKMIYKEAYFVKGNTESVSFEIDSINKEYIKKMKKKNY
KKEHMNKNNKDNNNNNNNSNKDDHININMNDNHRNYNDINLGPNSTDDSPTVSSLGNE
YTLDTYTSNNSDKEEIVKPLYKDTHEEFNKSSSMPFVKSSSMINNPSNFKYEDNSSS
FKGSISLETYLWYFQQVGFVLLTSVVIFMLISIFTDEIKFVFLTMMSIISKNNKEHSD
TILQKQVRYLEYFVILPIISLVTSGICFSMIIYGNITSAIKVHNNILYSILNAPLYIF
YNNNLGNIINRFIIDISAFDYGFLKRIYKAFFIFFRCILSSLLIIYMIRDCIFIFPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="ITS2 A-type"
/note="ribosomal operon internal
expressed in asexual stage parasi
27436. .31539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26045
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KKEEYENIHNSSNSTMSNEFKEKKKNNEYIIKLENCSFGLSYDNKCDNDHILKNINFN
LKRNSLAIIIGNVGSGKSAFFHSILGDFNMTHGNLYIENFFKKMPILYVPQNSWLFMG
NIRSMILFGNEYNPLIYKYTILQSELLNDLSTIEHGDMKYINDDHNLSKGQKVRICLA
RALYEHYIHMHKLCTDYEKKLIQPNEILDKDLINNKNISSYNNKKSKLVNYNIPFNEN
YLQKCLMDDNNFYLYLLDDIFTSLDPSISKKIFSNLFCKEDNISFKDNCSFIISMNKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTTYKENVGISNKGNKKKKSCQNISFLNFLSFDWIRPLINDLIKGDIQELPNICRNFDVPYYASKLEENLRDIEVEDSEFYSEKNSSNEHVLHHCNSNDASE KKVYNVYYHNILWSILKTFKFRIILIISFYILETLIVTLGGKFIDYYMRILEGQKIPV YISFLKDFKVFSGLVVMIMFFHLFFEALLHFYFHLFTINLKVSLMYFLYKINLCSNN NHLQNPDAFYNTYRKFSQTEIDEISRDFLSIGKNASSSSGIKNNNKNIDNNKFVEN DYIINFIKSTKKMEKDSLNENRSLPNVNIYNIMFSDVPSVTFFVTSCINLFNVFVKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26560
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                                                                                                                                                                                                                                                                                                                                                                                                             /note="28s rRNA expressed during asexual development"
complement(join(31966. .32476,32675. .32775))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEFKLIKMFNWESFAFKYINIFRMKEMKYCKIRLYLSNIGVFISSISSDIVEVVIFFI
YLKDRLNKKEEIKFTSIIMPLYVYKILISNVANFPNLVNNVMEGIVNIKRLNNYINDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parasites
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYYNDI KNYFMYRTRYNEDYNI VVDKTFLQNENI TSHDDGTSHNLKHLKNVI KNKLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="mall_5.8srNA"
26439. .26559
/gene="mall_5.8srNA"
/product="5.8s ribosomal RNA"
/note="5.8s ribosomal exppressed in asexual stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed in asexual stage 26439. .26559 'gene="mall_5.8srNA"
                                                                                                                                                                                                                                                                                                                                                                                  gene="MAL1P3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="ribosomal operon internal transcribed spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="28s ribosomal RNA (A-type)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="ITS1
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note="18s rRNA exppressed in asexual
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_xref="SPTREMBL:Q9U0N4"
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                                                      0;
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Pred. No. 0.00063;
); Mismatches 288;
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Query Match Best Local S Matches 312

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REFERENCE
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                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                   source
                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

E 1 (bases 1 to 249995)

S Gardner, M.J., Hall, N., Fung, E., White, O., Berriman, M., Hyman, R.W. Carlton, J.M., Pain, A., Nelson, K.E., Bowman, S., Paulsen, I.T., James, K., Eisen, J.A., Rutherford, K., Salzberg, S.L., Craig, A., Kyes, S., Chan, M.-S., Nene, V., Shallom, S.J., Suh, B., Peterson, J., Angiuoli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.M.A., Fairlamb, A.H., Fraunholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. & Barrell, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8535
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                                                                                                                                                       sequence of the human malaria parasite Plasmodium falciparum 419 (6906), 498-511 (2002)
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On Aug 12, 2000 this sequence ver * NOTE: This is a 'working draft'
TATTTGTATATATATATTTGTTTATTTGTTTTTGTATATATTTGTAAATATATTTGGAT
                            AAATCATTTTCAGAAAAGTAAATCATTTTTCAGAAATTATTTTTCGGAAATTATTTTACT
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                                                                 TATACATATGATTGTATATAATGAGACCACAAAATTAA---AAAATATAACATAATATA
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Yu,Y., Kim,H.R., Hatfield and Wing,R.
Sequencing of the maize g
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institut
University of Arizona
Biological Sciences West,
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.ariz
PCR PRimers
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ZMMBBb0284017.f ZMMBBb Zea mays subsp. mays genomic
ZMMBBb0284017 5', genomic survey sequence.
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             arizona.edu
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                                    Gossypium hirsutum (upland cotton)
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/db_xref="taxon:4578"
/clone="zMMBBb0284017"
/lab_host="DH10B"
/clone_lib="zMMBBb"
/note="Vector: pBeloBAC11; &
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:: rwing@clemson.edu
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/lab_host="E. coli"
/clone_lib="Gossypium hirsutum L."
/note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation, ordering clones and sequence analysis see
http://www.genome.clemson.edu/projects/stc/cotton/GH_MBb
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7885.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DH007DC06QP1&cluster=7885.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DH007DC06QP1.
Location/Qualifiers
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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Genoscope - Centre
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/organism="How"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODH007YF12"
/tissue_type="T CELLS (JURKAT CELL LINE)"
/cell_line="JURKAT CELL LINE"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned int the Not I and EcoRV sites of the pCMVSPORT 6 vector.

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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com l
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF022BB09QP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                   'note="Organ:
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Mammalia; Eutheria; P
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com 1
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP004AD10NP1.
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/db_xref="taxon:9606"
/clone="CS0CAP004YG19"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT_6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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P1 and ES
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Location/Qualifiers
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nation of this BAC-end sequence was
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/mol_type="genomic DNA"
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                     http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0CAP002AF05QP1&cluster=5393.f.Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation Faraday Avenue Genoscope sequence ID : CS0CAP002AF05QP1.
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertomammalia; Eutheria; Primates; Catarrhini; Horl (bases 1 to 1200)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                     Homo
                                                                               Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division o
Invitrogen. This sequence belongs to sequence cluster 5393
more information about this cluster, see
                                                                                                                                           Genoscope
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1197
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/clone lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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Pred. No. 8.9e-08;
L; Mismatches 218;
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Homo
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Contact: Genoscope
Genoscope - Centre
BP 191 91006 EVRY
                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 1200)
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S EVRY cedex - France
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Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com |
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP008BE02QP1.
Location/Qualifiers
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larity 40.7%;
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/clone lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com |
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF022BB09QP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPOR'
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mol_type="mRNA"

'db_xref="taxon:9606"

'clone="CSODF022YC18"
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Pred. No. 1.3e-07;
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BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
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AL069706.1 GI:4949849
GSS.
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Drosophila melanogaster
BACR29B23 of RPCI-98 lil
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larity 37.7%;
Conservative 10
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29B23"
/clone_lib="RPCI-98"
/note="end : T7"
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er genome survey sequence T7 end of BAC:
library from Drosophila melanogaster (fruit
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Pred. No. 2e-07;
7; Mismatches 225;
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segref@genoscope.cns.fr
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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
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06396.1 GI
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                                                                                                         AAGAATTAATGTTATTGGGATTACTAATTTCTAGTATTAATTGTGGTTTGGAAGTTAA
                                                                                                                                                                                       'AACTGTTTGGTGAAAATGTTAATGGTAGTGCTATGTCGAAGTATTTTCATGGAAGGTG
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larity 41.6%;
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note="end : T7"
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xref="taxon:7227"
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Pred. No. 2e-07;
Prematches 260;
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BX415058
3-PRIME,
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                                                                                                                                                                                                                                                                                                      Contact: Genoscope
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Library was constructed by L
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ilarity 38.1%;
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                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP004YG19"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned in
double-strand cDNA was digested with Not I and cloned in
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                                                                              nd EcoRV sites not normalized
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                    Score 114.8;
Pred. No. 3.3e
0; Mismatches
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Eukaryota;
Mammalia; F
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526 Homo sapiens PLACENTA COT 25-NORMALIZED Homo
CSODIO07YB08 5-PRIME, mRNA sequence.
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y was constructed by Life Technologies, a division of
ogen. Contact: Feng Liang Email: fliang@lifetech.com URL
/fulllength.invitrogen.com/ InVitroGen Corporation 1600
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gth cDNA libraries and
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               Eutheria;
                                                  mol_type="mRNA"
'db_xref="taxon:9606"
'clone="CS0DI007YB08"
tissue_type="PLACENTA COT 25-NORMALIZED"
clone_lib="Homo sapiens PLACENTA COT 25-
note="1st strand cDNA was primed with a
                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa;
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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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RESULT 14 BX437758/c LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	Db 4	Db x				D Qy	φ	Db S	dg 4d	Оу	Db 1	Query Ma Best Loc Matches	ORIGIN
BX437758 BX437758 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YB01 5-PRIME, mRNA sequence. BX437758 BX437758.1 GI:30773605 EST. Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1200) Li,W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France	759 TTGTCAAGTGATTTTGCTGTACTCACTACCTAGATTCTTATTTTCAGTATTGTAAAA 815 	0 1	TTAGAGAAACTAGAAATT	79 TCAGAAAAGTAAATCATTTTTCAGAAATTATTTTTCGGAAATT     :          :    :::::::::::::::::	20 TCAAACA-ATAGAAAATATTTTTTTGCAGGTTCATCCAAACACCC :	460 TAAAAAGATAATAAATTCTTAAATATATAAATTTTTTAAAATAGCTTTTCAGTAAATCTG 519   :	400 ТАТСТАААААТААТТТААААТАТАААТТТАТТААТАТАТАТААТАААСТСААТСАААСАА 459 	340 TAATATTTTAGTTTAATAATTGAGCATTATTATATATAATAAATA	281 TTTTATAACACAATTA-CAAATAATTTATTTAACTTTGGTTGTTTTCAATTTATGACGGT 339    :   :  : 	221 AGTATTAATTGTGGTTTGGAAGTTAATATATAATTATTCAATCCTTGTTTTTTATTTTTT 280 :	161 ATGTCGAAGTATTTTCATGGAAGGTGTTAAGAATTAATGTTATTGGGATTACTAATTTCT 220    :    :              ::::  :    :	14.0%; Score 114.6; DB 13; Length 1098; al Similarity 41.4%; Pred. No. 3.4e-07; 272; Conservative 78; Mismatches 305; Indels 2; Gaps 2;	sites of the pCMVSPORT 6 vector. Library was normalized."

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RESULT 15 BX439779/c LOCUS

DEFINITION

ACCESSION VERSION

BX439779 Hc BX439779 Hc 3-PRIME, mR BX439779 BX439779.1 EST.

GI:30771778

1201 bp r Homo sapiens PLACENTA Homo mRNA sequence.

mRNA

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CS0DE014YF05

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Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com |
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAPOO8CAO1QP1.
Location/Qualifiers
AWMAYATTTTTTTTTMTWAWAAAAAAAAAAATTTTTTTYYMYA
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Library was not normalized."
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Library was not normalized."
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46,	Sequence 2, A	quence 520	equence 254,	equence 225	equence 123,	eguence 1353,	equence 6381,	equence 536,	equence 144, Ap	equence 124,	equence 25	equence 13,	equence 59, Ap	equence 5738, A	equence 5686,	equence 1636,	, App	equence 958,	equence 12208,	nce 1	equence 16830,	Sequence 472, App	INFORMA	nce 2128	nce 58,	equence 38, Ap	equence 2	11234, A	Sequence 700, App

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7696, Application; Publication No. US200401233; GENERAL INFORMATION: APPLICANT: Deikman, Jill; APPLICANT: Feng, Paul C.C. APPLICANT: Fincher, Karer, APPLICANT: Ziegler, Todd
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 7696
LENGTH: 606
                                                                                                             Query Match 15.2%;
Best Local Similarity 82.9%;
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(606)
                                                                                                                                                                                                            LOCATION: (1)..(606)
OTHER INFORMATION: unsure at
OTHER INFORMATION: Clone ID:
246
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  TATATAATTATTCAATCCTTGTTTTTTTTTTTTTTTTTATAACACAATTACAAATAATT
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LIB3828-019-Q1-N6-D2
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                                                                                                              Score 124.2; DB 17; Pred. No. 7.6e-08; ); Mismatches 28;
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RESULT 3
US-10-312-841-1
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CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/2
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 7699
LENGTH: 520
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Sequence 7699, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
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Best Local
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APPLICANT:
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APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
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Pred. No. 0.0013;
Mismatches 174;
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RESULT 4 US-10-021-323-168

GENERAL

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Deikman, J Feng, Pau Fincher, Ziegler,

Paul C.C. er, Karen L. er, Todd E.

Publication Sequence

16830,

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e 16830, Application US/10021323 tion No. US20040123340A1 INFORMATION:

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LOCATION: (3
-10-312-841-1
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TION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
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ATION NUMBER: US/10/312,841
DATE: 2002-12-30
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Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                     FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2002-19-
PRIOR APPLICATION
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CURRENT APPLICATION NUMBER:
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                                                                                                        PRIOR
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  10-311-455-
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PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-12-14-14-NUMBER OF SEQ ID NOS: 17880
                                                                                                                      PRIOR
                                                         LENGTH:
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ORGANISM: Gossypium
                      FEATURE:
                                 ORGANISM: Artificial
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LENGTH: 469
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APPLICATION NUMBER: DE FILING DATE: 2000-09-01
OF SEQ ID NOS: 2424
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APPLICATION NUMBER: PCT/EP01/07537
FILING DATE: 2001-07-02
APPLICATION NUMBER: DE 10032529.7
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            INFORMATION:
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il Similarity 54.3%;
183; Conservative
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INVENTION: Diagnosis
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NUMBER OF SEQ
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TITLE OF INVENTION: Diagnosis
TITLE OF INVENTION: cytosine
FILE REFERENCE: 5013.1014
                                                                                                                                         CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
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                                  ORGANISM:
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CATION NUMBER: DE 10043826.1
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SEQ ID NOS: 2424
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Pred. No. 0.0056;
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US-10-433-793-114
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US-10-433-793-114
; Sequence 114, Ap
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EQ ID NO 114
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LENGTH: 6106
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NTE: 2000-09-01
D NOS: 540
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ON NUMBER: PCT/EP01/02955
TE: 2001-03-15
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PRIOR APPLICATION NUMBER: PCT/EP01/07537;
PRIOR FILING DATE: 2001-07-02;
PRIOR APPLICATION NUMBER: DE 10032529.7;
PRIOR FILING DATE: 2000-06-30;
PRIOR APPLICATION NUMBER: DE 10043826.1;
PRIOR FILING DATE: 2000-09-01;
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1445
                                                                                                                                                                                                                                                                                                                                                                     RESULT
   Query Match
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                                                                                                                                                                                                                  TITLE OF INVENTION: Cytosine FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE.
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DE 10043826.
PRIOR FILING DE 2000-06-30
2000-09-01
NUMBER OF SEQ SEQ ID NO 113
LENGTH: 6106
                                             Query Match
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Matches 278
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                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                   FILE REFERENCE: 5013.1011

CURRENT APPLICATION NUMBER: US/10/257,166

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: PCT/EP01/07470
                                                                                                                                                                                                                                                                                                APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Method and Nucleic Acids for Analysing
TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
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                   TTATTGGGATTACTAATTTCTAGTATTAATTGTGGTTTGGAAGTTAATATATAATTAT
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                                                                                                                                                                                                                   DATE:
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IEPENBROCK, C
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. US20040023230A1
TTCTATTTAGAGAAACTAGAAATTGATTTGTCAAATGTCTTTAATCTAGCTTGTTT 730
                                                                                                                                                                               NOS:
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                                           Score 89.4; DB 17; Pred. No. 0.0068; D; Mismatches 253;
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US-10-211-179-11/c

GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MORE
CURRENT APPLICATION NUMBER: US/
CURRENT FILING DATE: 2002-08-0
NUMBER OF SEQ ID NOS: 119
OTHER INFORMATION: n = a, t, o
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APPLICANT: Feng, Paul APPLICANT: Feng, Paul APPLICANT: Fincher, Karen L. APPLICANT: Ziegler, Todd E. TITLE OF INVENTION: Nucleic Acid Molecules an TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
TTLING DATE: 2000-12-14
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US-10-021-323-11125
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Publication No
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-10-021-323-1112
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EQ ID NO 11125
LENGTH: 565
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ORGANISM:
FEATURE:
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                                                                                                                                                                                              Application US/10021323
US20040123340A1
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                                                                                                                                                                                                                                                                                                                                                                                                        ID:
                                                                                                                                                                                                                                                                                                                                                                                                       LIB3828-034-Q6-N6-B10
                                                                                                                                                                                                                                                                                                                                            Score 89.2; DB 17; Pred. No. 0.0038; 0; Mismatches 193;
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APPLICANT: Feng, Paul C.C.

APPLICANT: Fincher, Karen L.

APPLICANT: Ziegler, Todd E.

TITLE OF INVENTION: Nucleic Acid Molecules a

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(52274)B

CURRENT APPLICATION NUMBER: US/10/021,323

CURRENT FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: US 60/255, 619

PRIOR FILING DATE: 2000-12-14

***TMMHER OF SEQ ID NOS: 17880
RESULT 14
US-10-021-323-2253
; Sequence 2253, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
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OTHER INFORMATION:
-0-021-323-7699
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APPLICANT:

Feng,

Paul

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FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
                   TITLE OF INVENTION: Diagnosis of Diseases A:
FILE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
                                                                                                                                                                                                                    ESULI 10-18-700 Sequence 700, Approximation No.
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Best Local S
Matches 207
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T: Ziegler, Todd E.

INVENTION: Nucleic Acid Molecules
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FENTION: Diagnosis
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iilarity 51.1%;
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Pred. No. 0.0051;
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ORGANISM: Artificial &
FEATURE:
OTHER INFORMATION: che
3-10-311-455-700
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Best Local Similarity 48.8%;

Matches 301; Conservative
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Pred. No. 0.013;
0; Mismatches 308;
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Search completed: September 20, 2004, 23:40:25 Job time : 479 secs